

SEQUENCE LISTING

<110> Saba, Julie D.
Fyrst, Henrik

<120> SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
POLYNUCLEOTIDES AND MODULATING AGENTS AND
METHODS OF USE THEREFOR

<130> 200116.402C2

<140> US

<141> 2002-01-17

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<170> FastSEQ for Windows Version 4.0

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<211> 1770

<212> DNA

<213> S. cerevisiae

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<221> CDS

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att cta acc atc aac gaa tta aaa ata gcc ata cat ggt tac ctc aga	144
Ile Leu Thr Ile Asn Glu Leu Lys Ile Ala Ile His Gly Tyr Leu Arg	
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aat acc cca tgg tac aac atg ttg aag gat tat ttg ttt gtg atc ttt	192
Asn Thr Pro Trp Tyr Asn Met Leu Lys Asp Tyr Leu Phe Val Ile Phe	
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Cys Tyr Lys Leu Ile Ser Asn Phe Phe Tyr Leu Leu Lys Val Tyr Gly	
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ccg gtg agg tta gca gtg aga aca tac gag cat agt tcc aga aga ttg	288
Pro Val Arg Leu Ala Val Arg Thr Tyr Glu His Ser Ser Arg Arg Leu	
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2002-01-17

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gaa gtc aca aag gtc aaa caa tcg atc gaa gac gaa cta att aga tcg	384
Glu Val Thr Lys Val Lys Gln Ser Ile Glu Asp Glu Leu Ile Arg Ser	
115 120 125	
gac tct cag tta atg aat ttc cca cag ttg cca tcc aat ggg ata cct	432
Asp Ser Gln Leu Met Asn Phe Pro Gln Leu Pro Ser Asn Gly Ile Pro	
130 135 140	
cag gat gat gtt att gaa gag cta aat aaa ttg aac gac ttg ata cca	480
Gln Asp Asp Val Ile Glu Glu Leu Asn Lys Leu Asn Asp Leu Ile Pro	
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His Thr Gln Trp Lys Glu Gly Lys Val Ser Gly Ala Val Tyr His Gly	
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Gly Asp Asp Leu Ile His Leu Gln Thr Ile Ala Tyr Glu Lys Tyr Cys	
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Val Ala Asn Gln Leu His Pro Asp Val Phe Pro Ala Val Arg Lys Met	
195 200 205	
gaa tcc gaa gtg gtt tct atg gtt tta aga atg ttt aat gcc cct tct	672
Glu Ser Glu Val Val Ser Met Val Leu Arg Met Phe Asn Ala Pro Ser	
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Asp Thr Gly Cys Gly Thr Thr Thr Ser Gly Gly Thr Glu Ser Leu Leu	
225 230 235 240	
tta gca tgt ctg agc gct aaa atg tat gcc ctt cat cat cgt gga atc	768
Leu Ala Cys Leu Ser Ala Lys Met Tyr Ala Leu His His Arg Gly Ile	
245 250 255	
acc gaa cca gaa ata att gct ccc gta act gca cat gct ggg ttt gac	816
Thr Glu Pro Glu Ile Ile Ala Pro Val Thr Ala His Ala Gly Phe Asp	
260 265 270	
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Lys Ala Ala Tyr Tyr Phe Gly Met Lys Leu Arg His Val Glu Leu Asp	
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Pro Thr Thr Tyr Gln Val Asp Leu Gly Lys Val Lys Lys Phe Ile Asn	
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1005510.01102

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 325 330 335
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 Pro Gly Val Thr Ser Ile Ser Cys Asp Thr His Lys Tyr Gly Phe Ala
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 cca aaa ggc tcg tca gtt ata atg tat aga aac agc gac tta cga atg 1200
 Pro Lys Gly Ser Ser Val Ile Met Tyr Arg Asn Ser Asp Leu Arg Met
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 His Gln Tyr Tyr Val Asn Pro Ala Trp Thr Gly Gly Leu Tyr Gly Ser
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 cct aca tta gca ggg tcc agg cct ggt gct att gtc gta ggt tgt tgg 1296
 Pro Thr Leu Ala Gly Ser Arg Pro Gly Ala Ile Val Val Gly Cys Trp
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 Ala Thr Met Val Asn Met Gly Glu Asn Gly Tyr Ile Glu Ser Cys Gln
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aaa act gct ggc gtt gca gac aaa ttg att gtg gga ttc cta gac gca 1728
 Lys Thr Ala Gly Val Ala Asp Lys Leu Ile Val Gly Phe Leu Asp Ala
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 Asn Thr Pro Trp Tyr Asn Met Leu Lys Asp Tyr Leu Phe Val Ile Phe
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 Cys Tyr Lys Leu Ile Ser Asn Phe Phe Tyr Leu Leu Lys Val Tyr Gly
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 Pro Val Arg Leu Ala Val Arg Thr Tyr Glu His Ser Ser Arg Arg Leu
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 Phe Arg Trp Leu Leu Asp Ser Pro Phe Leu Arg Gly Thr Val Glu Lys
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 Glu Val Thr Lys Val Lys Gln Ser Ile Glu Asp Glu Leu Ile Arg Ser
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 Asp Ser Gln Leu Met Asn Phe Pro Gln Leu Pro Ser Asn Gly Ile Pro
 130 135 140
 Gln Asp Asp Val Ile Glu Leu Asn Lys Leu Asn Asp Leu Ile Pro
 145 150 155 160
 His Thr Gln Trp Lys Glu Gly Lys Val Ser Gly Ala Val Tyr His Gly
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 Gly Asp Asp Leu Ile His Leu Gln Thr Ile Ala Tyr Glu Lys Tyr Cys
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 Val Ala Asn Gln Leu His Pro Asp Val Phe Pro Ala Val Arg Lys Met
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 Glu Ser Glu Val Val Ser Met Val Leu Arg Met Phe Asn Ala Pro Ser
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 Asp Thr Gly Cys Gly Thr Thr Thr Ser Gly Gly Thr Glu Ser Leu Leu

20251001055501

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 260 265 270
 Lys Ala Ala Tyr Tyr Phe Gly Met Lys Leu Arg His Val Glu Leu Asp
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 Pro Thr Thr Tyr Gln Val Asp Leu Gly Lys Val Lys Lys Phe Ile Asn
 290 295 300
 Lys Asn Thr Ile Leu Leu Val Gly Ser Ala Pro Asn Phe Pro His Gly
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 Met Glu Lys Ala Gly Tyr Lys Asn Leu Pro Leu Leu Asp Phe Arg Val
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 Pro Lys Gly Ser Ser Val Ile Met Tyr Arg Asn Ser Asp Leu Arg Met
 385 390 395 400
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 405 410 415
 Pro Thr Leu Ala Gly Ser Arg Pro Gly Ala Ile Val Val Gly Cys Trp
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 Ala Thr Met Val Asn Met Gly Glu Asn Gly Tyr Ile Glu Ser Cys Gln
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 Glu Ile Val Gly Ala Ala Met Lys Phe Lys Lys Tyr Ile Gln Glu Asn
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 485 490 495
 Lys Lys Gly Trp His Phe Asn Ala Leu Gln Lys Pro Val Ala Leu His
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 Ile Leu Arg Thr Thr Val Gln Glu Leu Lys Ser Glu Ser Asn Ser Lys
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Phe Glu Leu Arg Lys Phe Asn Pro Ile Val Leu Val Ser Ser Thr Ile	
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gtt gca aca tac gta ctc acc aat ctg aga cat atg cat tta gat gaa	144
Val Ala Thr Tyr Val Leu Thr Asn Leu Arg His Met His Leu Asp Glu	
35 40 45	
atg ggc atc cgg aaa cgt ttg agc act tgg ttt ttc acc act gta aag	192
Met Gly Ile Arg Lys Arg Leu Ser Thr Trp Phe Phe Thr Thr Val Lys	
50 55 60	
cgt gtg cct ttc atc agg aaa atg att gac aaa caa cta aac gaa gta	240
Arg Val Pro Phe Ile Arg Lys Met Ile Asp Lys Gln Leu Asn Glu Val	
65 70 75 80	
aag gac gag ctt gag aaa agt ctg aga att gtg gat cga agc acc gaa	288
Lys Asp Glu Leu Glu Lys Ser Leu Arg Ile Val Asp Arg Ser Thr Glu	
85 90 95	
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Tyr Phe Thr Thr Ile Pro Ser His Ser Val Gly Arg Thr Glu Val Leu	
100 105 110	
cgc ctt gct gcc atc tat gat gat ttg gaa gga cca gct ttt ttg gaa	384
Arg Leu Ala Ala Ile Tyr Asp Asp Leu Glu Gly Pro Ala Phe Leu Glu	
115 120 125	
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Gly Arg Val Ser Gly Ala Val Phe Asn Arg Glu Asp Asp Lys Asp Glu	
130 135 140	
cgg gag atg tat gag gag gtg ttc gga aaa ttt gcc tgg acc aac cca	480
Arg Glu Met Tyr Glu Glu Val Phe Gly Lys Phe Ala Trp Thr Asn Pro	
145 150 155 160	
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Leu Trp Pro Lys Leu Phe Pro Gly Val Arg Ile Met Glu Ala Glu Val	
165 170 175	
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Val Arg Met Cys Cys Asn Met Met Asn Gly Asp Ser Glu Thr Cys Gly	
180 185 190	
act atg tca act ggt gga tcc att tca att ctt ttg gcg tgc ctg gct	624
Thr Met Ser Thr Gly Gly Ser Ile Ser Ile Leu Leu Ala Cys Leu Ala	
195 200 205	

1055510 "0110" 2022

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225 230 235 240	
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Arg Ile Lys Val Arg Lys Ile Pro Val Asp Pro Val Thr Phe Lys Val	
245 250 255	
gac ctt gtc aaa atg aaa gcc gca att aac aag aga aca tgt atg tta	816
Asp Leu Val Lys Met Lys Ala Ala Ile Asn Lys Arg Thr Cys Met Leu	
260 265 270	
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Val Gly Ser Ala Pro Asn Phe Pro Phe Gly Thr Val Asp Asp Ile Glu	
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gct att gga cag cta gga ctt gaa tat gac atc cca gtt cat gtt gat	912
Ala Ile Gly Gln Leu Gly Leu Glu Tyr Asp Ile Pro Val His Val Asp	
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Ala Cys Leu Gly Gly Phe Leu Leu Pro Phe Leu Glu Glu Asp Glu Ile	
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Arg Tyr Asp Phe Arg Val Pro Gly Val Ser Ser Ile Ser Ala Asp Ser	
325 330 335	
cac aaa tac gga ctc gct cca aag ggg tca tca gtt gtt ctt tat cgc	1056
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aac att gca ctt tgc tgg gcc gca atg ctt tat cac gct cag gaa gga	1200
Asn Ile Ala Leu Cys Trp Ala Ala Met Leu Tyr His Ala Gln Glu Gly	
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Tyr Lys Ala Asn Ala Arg Lys Ile Val Asp Thr Thr Arg Lys Ile Arg	
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 450 455 460

ttc cca gct gga gtt cat atc atg gtc act atg aat cat act cat cct 1440
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gtc aaa agc cac aaa cca tcg gaa tcc gac aag aca agt gaa gca gcc 1536
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 65 70 75 80
 Lys Asp Glu Leu Glu Lys Ser Leu Arg Ile Val Asp Arg Ser Thr Glu
 85 90 95
 Tyr Phe Thr Thr Ile Pro Ser His Ser Val Gly Arg Thr Glu Val Leu
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 Arg Leu Ala Ala Ile Tyr Asp Asp Leu Glu Gly Pro Ala Phe Leu Glu

10053510.0102

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Arg	Tyr	Asp	Phe	Arg	Val	Pro	Gly	Val	Ser	Ser	Ile	Ser	Ala	Asp	Ser			
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Gly	Gly	Ile	Tyr	Ala	Ser	Ala	Thr	Met	Glu	Gly	Ser	Arg	Ala	Gly	His			
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 Cys Thr Leu Leu Ile Val Trp Val Tyr Glu Leu Ile Phe Gln Pro Glu
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 Met Pro Phe Ile Gly Arg Lys Ile Glu Gln Gln Val Ser Lys Ala Lys
 85 90 95

aag gat ctt gtc aag aac atg cca ttc cta aag gtg gac aag gat tat 336
 Lys Asp Leu Val Lys Asn Met Pro Phe Leu Lys Val Asp Lys Asp Tyr
 100 105 110

gtg aaa act ctg cct gct cag ggt atg ggc aca gct gag gtt ctg gag 384
 Val Lys Thr Leu Pro Ala Gln Gly Met Gly Thr Ala Glu Val Leu Glu
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 145 150 155 160

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ggg gga acg gaa agc atc ctg atg gcc tgc aaa gct tac cgg gac ttg 672
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 225 230 235 240

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 Ala His Ala Ala Phe Asp Lys Ala Ala His Tyr Phe Gly Met Lys Ile
 245 250 255

gtc cga gtt gca ctg aaa aag aac atg gag gtg gat gtg cag gca atg 816
 Val Arg Val Ala Leu Lys Lys Asn Met Glu Val Asp Val Gln Ala Met
 260 265 270

aag aga gcc atc tcc agg aac aca gct atg ctg gtc tgt tct acc cca 864
 Lys Arg Ala Ile Ser Arg Asn Thr Ala Met Leu Val Cys Ser Thr Pro
 275 280 285

cag ttt cct cat ggt gtg atg gat cct gtc ccc gaa gtg gcc aag tta 912
 Gln Phe Pro His Gly Val Met Asp Pro Val Pro Glu Val Ala Lys Leu
 290 295 300

act gtc aga tat aaa atc cca ctc cat gtg gat gct tgt ctg ggg ggc 960
 Thr Val Arg Tyr Lys Ile Pro Leu His Val Asp Ala Cys Leu Gly Gly
 305 310 315 320

ttc ctc att gtc ttc atg gag aaa gca ggg tac cca ctg gag aaa cca 1008
 Phe Leu Ile Val Phe Met Glu Lys Ala Gly Tyr Pro Leu Glu Lys Pro
 325 330 335

ttt gat ttc cgg gtg aaa ggt gtg acc agc att tca gca gat act cat 1056
 Phe Asp Phe Arg Val Lys Gly Val Thr Ser Ile Ser Ala Asp Thr His
 340 345 350

aag tat ggc tat gct cct aaa ggt tca tca gtg gtg atg tac tct aac 1104
 Lys Tyr Gly Tyr Ala Pro Lys Gly Ser Ser Val Val Met Tyr Ser Asn
 355 360 365

gag aag tac agg acg tac cag ttc ttt gtt ggt gca gac tgg caa ggt 1152
 Glu Lys Tyr Arg Thr Tyr Gln Phe Phe Val Gly Ala Asp Trp Gln Gly
 370 375 380

ggt gtc tac gca tct cca agc ata gct ggc tca cgg cct ggt ggc atc 1200

10055510 01303
 20210 0155007

Gly Val Tyr Ala Ser Pro Ser Ile Ala Gly Ser Arg Pro Gly Gly Ile
 385 390 395 400
 att gca gcc tgt tgg gcg gcc ttg atg cac ttc ggt gag aac ggc tat 1248
 Ile Ala Ala Cys Trp Ala Ala Leu Met His Phe Gly Glu Asn Gly Tyr
 405 410 415
 gtt gaa gct acc aaa cag atc atc aaa act gct cgc ttc ctg aag tca 1296
 Val Glu Ala Thr Lys Gln Ile Ile Lys Thr Ala Arg Phe Leu Lys Ser
 420 425 430
 gaa ctg gaa aac atc aaa aac atc ttc att ttc ggt gat cct caa ttg 1344
 Glu Leu Glu Asn Ile Lys Asn Ile Phe Ile Phe Gly Asp Pro Gln Leu
 435 440 445
 tca gtt att gct ctg gga tcc aac gat ttt gac att tac cga cta tct 1392
 Ser Val Ile Ala Leu Gly Ser Asn Asp Phe Asp Ile Tyr Arg Leu Ser
 450 455 460
 aat atg atg tct gct aag ggg tgg aat ttt aac tac ctg cag ttc cca 1440
 Asn Met Met Ser Ala Lys Gly Trp Asn Phe Asn Tyr Leu Gln Phe Pro
 465 470 475 480
 aga agc att cat ttc tgc att acg tta gta cat act cgg aag cga gtg 1488
 Arg Ser Ile His Phe Cys Ile Thr Leu Val His Thr Arg Lys Arg Val
 485 490 495
 gcg atc cag ttc cta aag gat atc cgg gaa tca gtc aca caa atc atg 1536
 Ala Ile Gln Phe Leu Lys Asp Ile Arg Glu Ser Val Thr Gln Ile Met
 500 505 510
 aag aat cct aaa gct aag acc aca gga atg ggt gcc atc tat ggc atg 1584
 Lys Asn Pro Lys Ala Lys Thr Thr Gly Met Gly Ala Ile Tyr Gly Met
 515 520 525
 gcc cag gca acc att gac agg aag ctg gtt gca gaa ata tcc tcc gtc 1632
 Ala Gln Ala Thr Ile Asp Arg Lys Leu Val Ala Glu Ile Ser Ser Val
 530 535 540
 ttc ttg gac tgc ctt tat act acg gac ccc gtg act cag ggc aac cag 1680
 Phe Leu Asp Cys Leu Tyr Thr Thr Asp Pro Val Thr Gln Gly Asn Gln
 545 550 555 560
 atg aac ggt tct cca aag ccc cgc tga 1707
 Met Asn Gly Ser Pro Lys Pro Arg *
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 <400> 6

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 20 25 30
 Tyr Cys Thr Lys Tyr Glu Pro Trp Gln Leu Ile Ala Trp Ser Val Leu
 35 40 45
 Cys Thr Leu Leu Ile Val Trp Val Tyr Glu Leu Ile Phe Gln Pro Glu
 50 55 60
 Ser Leu Trp Ser Arg Phe Lys Lys Lys Leu Phe Lys Leu Ile Arg Lys
 65 70 75 80
 Met Pro Phe Ile Gly Arg Lys Ile Glu Gln Gln Val Ser Lys Ala Lys
 85 90 95
 Lys Asp Leu Val Lys Asn Met Pro Phe Leu Lys Val Asp Lys Asp Tyr
 100 105 110
 Val Lys Thr Leu Pro Ala Gln Gly Met Gly Thr Ala Glu Val Leu Glu
 115 120 125
 Arg Leu Lys Glu Tyr Ser Ser Met Asp Gly Ser Trp Gln Glu Gly Lys
 130 135 140
 Ala Ser Gly Ala Val Tyr Asn Gly Glu Pro Lys Leu Thr Glu Leu Leu
 145 150 155 160
 Val Gln Ala Tyr Gly Glu Phe Thr Trp Ser Asn Pro Leu His Pro Asp
 165 170 175
 Ile Phe Pro Gly Leu Arg Lys Leu Glu Ala Glu Ile Val Arg Met Thr
 180 185 190
 Cys Ser Leu Phe Asn Gly Gly Pro Asp Ser Cys Gly Cys Val Thr Ser
 195 200 205
 Gly Gly Thr Glu Ser Ile Leu Met Ala Cys Lys Ala Tyr Arg Asp Leu
 210 215 220
 Ala Leu Glu Lys Gly Ile Lys Thr Pro Glu Ile Val Ala Pro Glu Ser
 225 230 235 240
 Ala His Ala Ala Phe Asp Lys Ala Ala His Tyr Phe Gly Met Lys Ile
 245 250 255
 Val Arg Val Ala Leu Lys Lys Asn Met Glu Val Asp Val Gln Ala Met
 260 265 270
 Lys Arg Ala Ile Ser Arg Asn Thr Ala Met Leu Val Cys Ser Thr Pro
 275 280 285
 Gln Phe Pro His Gly Val Met Asp Pro Val Pro Glu Val Ala Lys Leu
 290 295 300
 Thr Val Arg Tyr Lys Ile Pro Leu His Val Asp Ala Cys Leu Gly Gly
 305 310 315 320
 Phe Leu Ile Val Phe Met Glu Lys Ala Gly Tyr Pro Leu Glu Lys Pro
 325 330 335
 Phe Asp Phe Arg Val Lys Gly Val Thr Ser Ile Ser Ala Asp Thr His
 340 345 350
 Lys Tyr Gly Tyr Ala Pro Lys Gly Ser Ser Val Val Met Tyr Ser Asn
 355 360 365
 Glu Lys Tyr Arg Thr Tyr Gln Phe Phe Val Gly Ala Asp Trp Gln Gly
 370 375 380
 Gly Val Tyr Ala Ser Pro Ser Ile Ala Gly Ser Arg Pro Gly Gly Ile
 385 390 395 400
 Ile Ala Ala Cys Trp Ala Ala Leu Met His Phe Gly Glu Asn Gly Tyr
 405 410 415
 Val Glu Ala Thr Lys Gln Ile Ile Lys Thr Ala Arg Phe Leu Lys Ser
 420 425 430

10053510 "011702"

Glu Leu Glu Asn Ile Lys Asn Ile Phe Ile Phe Gly Asp Pro Gln Leu
 435 440 445
 Ser Val Ile Ala Leu Gly Ser Asn Asp Phe Asp Ile Tyr Arg Leu Ser
 450 455 460
 Asn Met Met Ser Ala Lys Gly Trp Asn Phe Asn Tyr Leu Gln Phe Pro
 465 470 475 480
 Arg Ser Ile His Phe Cys Ile Thr Leu Val His Thr Arg Lys Arg Val
 485 490 495
 Ala Ile Gln Phe Leu Lys Asp Ile Arg Glu Ser Val Thr Gln Ile Met
 500 505 510
 Lys Asn Pro Lys Ala Lys Thr Thr Gly Met Gly Ala Ile Tyr Gly Met
 515 520 525
 Ala Gln Ala Thr Ile Asp Arg Lys Leu Val Ala Glu Ile Ser Ser Val
 530 535 540
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 Met Asn Gly Ser Pro Lys Pro Arg
 565

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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (1)...(1707)

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 gag att ttg gaa gta tac tcc aca aaa gcc aag aat tat gta aat gga 96
 Glu Ile Leu Glu Val Tyr Ser Thr Lys Ala Lys Asn Tyr Val Asn Gly
 20 25 30

 cat tgc acc aag tat gag ccc tgg cag cta att gca tgg agt gtc gtg 144
 His Cys Thr Lys Tyr Glu Pro Trp Gln Leu Ile Ala Trp Ser Val Val
 35 40 45

 tgg acc ctg ctg ata gtc tgg gga tat gag ttt gtc ttc cag cca gag 192
 Trp Thr Leu Leu Ile Val Trp Gly Tyr Glu Phe Val Phe Gln Pro Glu
 50 55 60

 agt tta tgg tca agg ttt aaa aag aaa tgt ttt aag ctc acc agg aag 240
 Ser Leu Trp Ser Arg Phe Lys Lys Lys Cys Phe Lys Leu Thr Arg Lys
 65 70 75 80

 atg ccc att att ggt cgt aag att caa gac aag ttg aac aag acc aag 288
 Met Pro Ile Ile Gly Arg Lys Ile Gln Asp Lys Leu Asn Lys Thr Lys
 85 90 95

gat gat att agc aag aac atg tca ttc ctg aaa gtg gac aaa gag tat 336
 Asp Asp Ile Ser Lys Asn Met Ser Phe Leu Lys Val Asp Lys Glu Tyr
 100 105 110

gtg aaa gct tta ccc tcc cag ggt ctg agc tca tct gct gtt ttg gag 384
 Val Lys Ala Leu Pro Ser Gln Gly Leu Ser Ser Ser Ala Val Leu Glu
 115 120 125

aaa ctt aag gag tac agc tct atg gac gcc ttc tgg caa gag ggg aga 432
 Lys Leu Lys Glu Tyr Ser Ser Met Asp Ala Phe Trp Gln Glu Gly Arg
 130 135 140

gcc tct gga aca gtg tac agt ggg gag gag aag ctc act gag ctc ctt 480
 Ala Ser Gly Thr Val Tyr Ser Gly Glu Glu Lys Leu Thr Glu Leu Leu
 145 150 155 160

gtg aag gct tat gga gat ttt gca tgg agt aac ccc ctg cat cca gat 528
 Val Lys Ala Tyr Gly Asp Phe Ala Trp Ser Asn Pro Leu His Pro Asp
 165 170 175

atc ttc cca gga cta cgc aag ata gag gca gaa att gtg agg ata gct 576
 Ile Phe Pro Gly Leu Arg Lys Ile Glu Ala Glu Ile Val Arg Ile Ala
 180 185 190

tgt tcc ctg ttc aat ggg gga cca gat tcg tgt gga tgt gtg act tct 624
 Cys Ser Leu Phe Asn Gly Gly Pro Asp Ser Cys Gly Cys Val Thr Ser
 195 200 205

ggg gga aca gaa agc ata ctc atg gcc tgc aaa gca tgt cgg gat ctg 672
 Gly Gly Thr Glu Ser Ile Leu Met Ala Cys Lys Ala Cys Arg Asp Leu
 210 215 220

gcc ttt gag aag ggg atc aaa act cca gaa att gtg gct ccc caa agt 720
 Ala Phe Glu Lys Gly Ile Lys Thr Pro Glu Ile Val Ala Pro Gln Ser
 225 230 235 240

gcc cat gct gca ttt aac aaa gca gcc agt tac ttt ggg atg aag att 768
 Ala His Ala Ala Phe Asn Lys Ala Ala Ser Tyr Phe Gly Met Lys Ile
 245 250 255

gtg cgg gtc cca ttg acg aag atg atg gag gtg gat gtg agg gca atg 816
 Val Arg Val Pro Leu Thr Lys Met Met Glu Val Asp Val Arg Ala Met
 260 265 270

aga aga gct atc tcc agg aac act gcc atg ctc gtc tgt tct acc cca 864
 Arg Arg Ala Ile Ser Arg Asn Thr Ala Met Leu Val Cys Ser Thr Pro
 275 280 285

cag ttt cct cat ggt gta ata gat cct gtc cct gaa gtg gcc aag ctg 912
 Gln Phe Pro His Gly Val Ile Asp Pro Val Pro Glu Val Ala Lys Leu
 290 295 300

gct gtc aaa tac aaa ata ccc ctt cat gtc gac gct tgt ctg gga ggc 960
 Ala Val Lys Tyr Lys Ile Pro Leu His Val Asp Ala Cys Leu Gly Gly

1005310 04403
 20270 045500T

305	310	315	320	
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Phe Leu Ile Val Phe Met Glu Lys Ala Gly Tyr Pro Leu Glu His Pro				
325 330 335				
ttt gat ttc cgg gtg aaa ggt gta acc agc att tca gct gac acc cat	1056			
Phe Asp Phe Arg Val Lys Gly Val Thr Ser Ile Ser Ala Asp Thr His				
340 345 350				
aag tat ggc tat gcc cca aaa ggc tca tca ttg gtg ttg tat agt gac	1104			
Lys Tyr Gly Tyr Ala Pro Lys Gly Ser Ser Leu Val Leu Tyr Ser Asp				
355 360 365				
aag aag tac agg aac tat cag ttc ttc gtc gat aca gat tgg cag ggt	1152			
Lys Lys Tyr Arg Asn Tyr Gln Phe Phe Val Asp Thr Asp Trp Gln Gly				
370 375 380				
ggc atc tat gct tcc cca acc atc gca ggc tca cgg cct ggt ggc att	1200			
Gly Ile Tyr Ala Ser Pro Thr Ile Ala Gly Ser Arg Pro Gly Gly Ile				
385 390 395 400				
agc gca gcc tgt tgg gct gcc ttg atg cac ttc ggt gag aac ggc tat	1248			
Ser Ala Ala Cys Trp Ala Ala Leu Met His Phe Gly Glu Asn Gly Tyr				
405 410 415				
gtt gaa gct acc aaa cag atc atc aaa act gct cgc ttc ctc aag tca	1296			
Val Glu Ala Thr Lys Gln Ile Ile Lys Thr Ala Arg Phe Leu Lys Ser				
420 425 430				
gaa ctg gaa aat atc aaa ggc atc ttt gtt ttt ggg aat ccc caa ttg	1344			
Glu Leu Glu Asn Ile Lys Gly Ile Phe Val Phe Gly Asn Pro Gln Leu				
435 440 445				
tca ctc att gct ctg gga tcc cgt gat ttt gac atc tac cga cta tca	1392			
Ser Leu Ile Ala Leu Gly Ser Arg Asp Phe Asp Ile Tyr Arg Leu Ser				
450 455 460				
aac ctg atg act gct aag ggg tgg aac ttg aac cag ttg cag ttc cca	1440			
Asn Leu Met Thr Ala Lys Gly Trp Asn Leu Asn Gln Leu Gln Phe Pro				
465 470 475 480				
ccc agt att cat ttc tgc atc aca tta cta cac gcc cgg aaa cga gta	1488			
Pro Ser Ile His Phe Cys Ile Thr Leu Leu His Ala Arg Lys Arg Val				
485 490 495				
gct ata caa ttc cta aag gac att cga gaa tct gtc act caa atc atg	1536			
Ala Ile Gln Phe Leu Lys Asp Ile Arg Glu Ser Val Thr Gln Ile Met				
500 505 510				
aag aat cct aaa gcg aag acc aca gga atg ggt gcc atc tat gcc atg	1584			
Lys Asn Pro Lys Ala Lys Thr Thr Gly Met Gly Ala Ile Tyr Ala Met				
515 520 525				

10053510 0440E

gcc cag aca act gtt gac agg aat atg gtt gca gaa ttg tcc tca gtc 1632
 Ala Gln Thr Thr Val Asp Arg Asn Met Val Ala Glu Leu Ser Ser Val
 530 535 540

ttc ttg gac agc ttg tac agc acc gac act gtc acc cag ggc agc cag 1680
 Phe Leu Asp Ser Leu Tyr Ser Thr Asp Thr Val Thr Gln Gly Ser Gln
 545 550 555 560

atg aat ggt tct cca aaa ccc cac tga 1707
 Met Asn Gly Ser Pro Lys Pro His *
 565

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 <211> 568
 <212> PRT
 <213> Homo sapiens

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 His Cys Thr Lys Tyr Glu Pro Trp Gln Leu Ile Ala Trp Ser Val Val
 35 40 45
 Trp Thr Leu Leu Ile Val Trp Gly Tyr Glu Phe Val Phe Gln Pro Glu
 50 55 60
 Ser Leu Trp Ser Arg Phe Lys Lys Lys Cys Phe Lys Leu Thr Arg Lys
 65 70 75 80
 Met Pro Ile Ile Gly Arg Lys Ile Gln Asp Lys Leu Asn Lys Thr Lys
 85 90 95
 Asp Asp Ile Ser Lys Asn Met Ser Phe Leu Lys Val Asp Lys Glu Tyr
 100 105 110
 Val Lys Ala Leu Pro Ser Gln Gly Leu Ser Ser Ser Ala Val Leu Glu
 115 120 125
 Lys Leu Lys Glu Tyr Ser Ser Met Asp Ala Phe Trp Gln Glu Gly Arg
 130 135 140
 Ala Ser Gly Thr Val Tyr Ser Gly Glu Glu Lys Leu Thr Glu Leu Leu
 145 150 155 160
 Val Lys Ala Tyr Gly Asp Phe Ala Trp Ser Asn Pro Leu His Pro Asp
 165 170 175
 Ile Phe Pro Gly Leu Arg Lys Ile Glu Ala Glu Ile Val Arg Ile Ala
 180 185 190
 Cys Ser Leu Phe Asn Gly Gly Pro Asp Ser Cys Gly Cys Val Thr Ser
 195 200 205
 Gly Gly Thr Glu Ser Ile Leu Met Ala Cys Lys Ala Cys Arg Asp Leu
 210 215 220
 Ala Phe Glu Lys Gly Ile Lys Thr Pro Glu Ile Val Ala Pro Gln Ser
 225 230 235 240
 Ala His Ala Ala Phe Asn Lys Ala Ala Ser Tyr Phe Gly Met Lys Ile
 245 250 255
 Val Arg Val Pro Leu Thr Lys Met Met Glu Val Asp Val Arg Ala Met
 260 265 270
 Arg Arg Ala Ile Ser Arg Asn Thr Ala Met Leu Val Cys Ser Thr Pro

202510.01202

275 280 285
 Gln Phe Pro His Gly Val Ile Asp Pro Val Pro Glu Val Ala Lys Leu
 290 295 300
 Ala Val Lys Tyr Lys Ile Pro Leu His Val Asp Ala Cys Leu Gly Gly
 305 310 315 320
 Phe Leu Ile Val Phe Met Glu Lys Ala Gly Tyr Pro Leu Glu His Pro
 325 330 335
 Phe Asp Phe Arg Val Lys Gly Val Thr Ser Ile Ser Ala Asp Thr His
 340 345 350
 Lys Tyr Gly Tyr Ala Pro Lys Gly Ser Ser Leu Val Leu Tyr Ser Asp
 355 360 365
 Lys Lys Tyr Arg Asn Tyr Gln Phe Phe Val Asp Thr Asp Trp Gln Gly
 370 375 380
 Gly Ile Tyr Ala Ser Pro Thr Ile Ala Gly Ser Arg Pro Gly Gly Ile
 385 390 395 400
 Ser Ala Ala Cys Trp Ala Ala Leu Met His Phe Gly Glu Asn Gly Tyr
 405 410 415
 Val Glu Ala Thr Lys Gln Ile Ile Lys Thr Ala Arg Phe Leu Lys Ser
 420 425 430
 Glu Leu Glu Asn Ile Lys Gly Ile Phe Val Phe Gly Asn Pro Gln Leu
 435 440 445
 Ser Leu Ile Ala Leu Gly Ser Arg Asp Phe Asp Ile Tyr Arg Leu Ser
 450 455 460
 Asn Leu Met Thr Ala Lys Gly Trp Asn Leu Asn Gln Leu Gln Phe Pro
 465 470 475 480
 Pro Ser Ile His Phe Cys Ile Thr Leu Leu His Ala Arg Lys Arg Val
 485 490 495
 Ala Ile Gln Phe Leu Lys Asp Ile Arg Glu Ser Val Thr Gln Ile Met
 500 505 510
 Lys Asn Pro Lys Ala Lys Thr Thr Gly Met Gly Ala Ile Tyr Ala Met
 515 520 525
 Ala Gln Thr Thr Val Asp Arg Asn Met Val Ala Glu Leu Ser Ser Val
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 545 550 555 560
 Met Asn Gly Ser Pro Lys Pro His
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 <212> DNA
 <213> Homo sapiens

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 gag att ttg gaa gta tac tcc aca aaa gcc aag aat tat gta aat gga 96

Glu	Ile	Leu	Glu	Val	Tyr	Ser	Thr	Lys	Ala	Lys	Asn	Tyr	Val	Asn	Gly	
			20				25						30			
cat	tgc	acc	aag	tat	gag	ccc	tgg	cag	cta	att	gca	tgg	agt	gtc	gtg	144
His	Cys	Thr	Lys	Tyr	Glu	Pro	Trp	Gln	Leu	Ile	Ala	Trp	Ser	Val	Val	
			35				40						45			
tgg	acc	ctg	ctg	ata	gtc	tgg	gga	tat	gag	ttt	gtc	ttc	cag	cca	gag	192
Trp	Thr	Leu	Leu	Ile	Val	Trp	Gly	Tyr	Glu	Phe	Val	Phe	Gln	Pro	Glu	
			50				55						60			
agt	tta	tgg	tca	agg	ttt	aaa	aag	aaa	tgt	ttt	aag	ctc	acc	agg	aag	240
Ser	Leu	Trp	Ser	Arg	Phe	Lys	Lys	Lys	Cys	Phe	Lys	Leu	Thr	Arg	Lys	
			65				70						75	80		
atg	ccc	att	att	ggc	cgt	aag	att	caa	gac	aag	ttg	aac	aag	acc	aag	288
Met	Pro	Ile	Ile	Gly	Arg	Lys	Ile	Gln	Asp	Lys	Leu	Asn	Lys	Thr	Lys	
			85				90						95			
gat	gat	att	agc	aag	aac	atg	tca	ttc	ctg	aaa	gtg	gac	aaa	gag	tat	336
Asp	Asp	Ile	Ser	Lys	Asn	Met	Ser	Phe	Leu	Lys	Val	Asp	Lys	Glu	Tyr	
			100				105						110			
gtg	aaa	gct	tta	ccc	tcc	cag	ggc	ctg	agc	tca	tct	gct	gtt	ttg	gag	384
Val	Lys	Ala	Leu	Pro	Ser	Gln	Gly	Leu	Ser	Ser	Ser	Ala	Val	Leu	Glu	
			115				120						125			
aaa	ctt	aag	gag	tac	agc	tct	atg	gac	gcc	ttc	tgg	caa	gag	ggg	aga	432
Lys	Leu	Lys	Glu	Tyr	Ser	Ser	Met	Asp	Ala	Phe	Trp	Gln	Glu	Gly	Arg	
			130				135						140			
gcc	tct	gga	aca	gtg	tac	agt	ggg	gag	gag	aag	ctc	act	gag	ctc	ctt	480
Ala	Ser	Gly	Thr	Val	Tyr	Ser	Gly	Glu	Glu	Lys	Leu	Thr	Glu	Leu	Leu	
			145				150						155	160		
gtg	aag	gct	tat	gga	gat	ttt	gca	tgg	agt	aac	ccc	ctg	cat	cca	gat	528
Val	Lys	Ala	Tyr	Gly	Asp	Phe	Ala	Trp	Ser	Asn	Pro	Leu	His	Pro	Asp	
			165				170						175			
atc	ttc	cca	gga	cta	cgc	aag	ata	gag	gca	gaa	att	gtg	agg	ata	gct	576
Ile	Phe	Pro	Gly	Leu	Arg	Lys	Ile	Glu	Ala	Glu	Ile	Val	Arg	Ile	Ala	
			180				185						190			
tgt	tcc	ctg	ttc	aat	ggg	gga	cca	gat	tcg	tgt	gga	tgt	gtg	act	tct	624
Cys	Ser	Leu	Phe	Asn	Gly	Gly	Pro	Asp	Ser	Cys	Gly	Cys	Val	Thr	Ser	
			195				200						205			
ggg	gga	aca	gaa	agc	ata	ctc	atg	gcc	tgc	aaa	gca	tgt	cgg	gat	ctg	672
Gly	Gly	Thr	Glu	Ser	Ile	Leu	Met	Ala	Cys	Lys	Ala	Cys	Arg	Asp	Leu	
			210				215						220			
gcc	ttt	gag	aag	ggg	atc	aaa	act	cca	gaa	att	gtg	gct	ccc	caa	agt	720
Ala	Phe	Glu	Lys	Gly	Ile	Lys	Thr	Pro	Glu	Ile	Val	Ala	Pro	Gln	Ser	
			225				230						235	240		

gcc cat gct gca ttt aac aaa gca gcc agt tac ttt ggg atg aag att 768
 Ala His Ala Ala Phe Asn Lys Ala Ala Ser Tyr Phe Gly Met Lys Ile
 245 250 255

gtg cgg gtc cca ttg acg aag atg atg gag gtg gat gtg agg gca atg 816
 Val Arg Val Pro Leu Thr Lys Met Met Glu Val Asp Val Arg Ala Met
 260 265 270

aga aga gct atc tcc agg aac act gcc atg ctc gtc tgt tct acc cca 864
 Arg Arg Ala Ile Ser Arg Asn Thr Ala Met Leu Val Cys Ser Thr Pro
 275 280 285

cag ttt cct cat ggt gta ata gat cct gtc cct gaa gtg gcc aag ctg 912
 Gln Phe Pro His Gly Val Ile Asp Pro Val Pro Glu Val Ala Lys Leu
 290 295 300

gct gtc aaa tac aaa ata ccc ctt cat gtc gac gct tgt ctg gga ggc 960
 Ala Val Lys Tyr Lys Ile Pro Leu His Val Asp Ala Cys Leu Gly Gly
 305 310 315 320

ttc ctc atc gtc ttt atg gag aaa gca gga tac cca ctg gag cac cca 1008
 Phe Leu Ile Val Phe Met Glu Lys Ala Gly Tyr Pro Leu Glu His Pro
 325 330 335

ttt gat ttc cgg gtg aaa ggt gta acc agc att tca gct gac acc cat 1056
 Phe Asp Phe Arg Val Lys Gly Val Thr Ser Ile Ser Ala Asp Thr His
 340 345 350

aag ctg gaa aat atc aaa ggc atc ttt gtt ttt ggg aat ccc caa ttg 1104
 Lys Leu Glu Asn Ile Lys Gly Ile Phe Val Phe Gly Asn Pro Gln Leu
 355 360 365

tca ctc att gct ctg gga tcc cgt gat ttt gac atc tac cga cta tca 1152
 Ser Leu Ile Ala Leu Gly Ser Arg Asp Phe Asp Ile Tyr Arg Leu Ser
 370 375 380

aac ctg atg act gct aag ggg tgg aac ttg aac cag ttg cag ttc cca 1200
 Asn Leu Met Thr Ala Lys Gly Trp Asn Leu Asn Gln Leu Gln Phe Pro
 385 390 395 400

ccc agt att cat ttc tgc atc aca tta cta cac gcc cgg aaa cga gta 1248
 Pro Ser Ile His Phe Cys Ile Thr Leu Leu His Ala Arg Lys Arg Val
 405 410 415

gct ata caa ttc cta aag gac att cga gaa tct gtc act caa atc atg 1296
 Ala Ile Gln Phe Leu Lys Asp Ile Arg Glu Ser Val Thr Gln Ile Met
 420 425 430

aag aat cct aaa gcg aag acc aca gga atg ggt gcc atc tat gcc atg 1344
 Lys Asn Pro Lys Ala Lys Thr Thr Gly Met Gly Ala Ile Tyr Ala Met
 435 440 445

gcc cag aca act gtt gac agg aat atg gtt gca gaa ttg tcc tca gtc 1392

1005510.0170
 20210705

Ala Gln Thr Thr Val Asp Arg Asn Met Val Ala Glu Leu Ser Ser Val
 450 455 460

ttc ttg gac agc ttg tac agc acc gac act gtc acc cag ggc agc cag 1440
 Phe Leu Asp Ser Leu Tyr Ser Thr Asp Thr Val Thr Gln Gly Ser Gln
 465 470 475 480

atg aat ggt tct cca aaa ccc cac tga 1467
 Met Asn Gly Ser Pro Lys Pro His *

485

<210> 10
 <211> 488
 <212> PRT
 <213> Homo sapiens

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Lys	Tyr	Gly	Tyr	Ala	Pro	Lys	Gly	Ser	Ser	Leu	Val	Leu	Tyr	Ser	Asp	
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aag	aag	tac	agg	aac	tat	cag	ttc	ttc	gtc	gat	aca	gat	tgg	cag	ggg	1152
Lys	Lys	Tyr	Arg	Asn	Tyr	Gln	Phe	Phe	Val	Asp	Thr	Asp	Trp	Gln	Gly	
	370					375					380					
ggc	atc	tat	gct	tcc	cca	acc	atc	gca	ggc	tca	cgg	cct	ggg	ggc	att	1200
Gly	Ile	Tyr	Ala	Ser	Pro	Thr	Ile	Ala	Gly	Ser	Arg	Pro	Gly	Gly	Ile	
385					390					395					400	
agc	gca	gcc	tgt	tgg	gct	gcc	ttg	atg	cac	ttc	ggg	gag	aac	ggc	tat	1248
Ser	Ala	Ala	Cys	Trp	Ala	Ala	Leu	Met	His	Phe	Gly	Glu	Asn	Gly	Tyr	
				405					410					415		
gtt	gaa	gct	acc	aaa	cag	atc	atc	aaa	act	gct	cgc	ttc	ctc	aag	tca	1296
Val	Glu	Ala	Thr	Lys	Gln	Ile	Ile	Lys	Thr	Ala	Arg	Phe	Leu	Lys	Ser	
			420					425					430			
gaa	ctg	gaa	aat	atc	aaa	ggc	atc	ttt	gtt	ttt	ggg	aat	ccc	caa	ttg	1344
Glu	Leu	Glu	Asn	Ile	Lys	Gly	Ile	Phe	Val	Phe	Gly	Asn	Pro	Gln	Leu	
		435					440					445				
tca	gtc	att	gct	ctg	gga	tcc	cgt	gat	ttt	gac	atc	tac	cga	cta	tca	1392
Ser	Val	Ile	Ala	Leu	Gly	Ser	Arg	Asp	Phe	Asp	Ile	Tyr	Arg	Leu	Ser	
	450					455					460					
aac	ctg	atg	act	gct	aag	ggg	tgg	aac	ttg	aac	cag	ttg	cag	ttc	cca	1440
Asn	Leu	Met	Thr	Ala	Lys	Gly	Trp	Asn	Leu	Asn	Gln	Leu	Gln	Phe	Pro	
465					470					475					480	
ccc	agt	att	cat	ttc	tgc	atc	aca	tta	cta	cac	gcc	cgg	aaa	cga	gta	1488

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Pro Ser Ile His Phe Cys Ile Thr Leu Leu His Ala Arg Lys Arg Val
 485 490 495

gct ata caa ttc cta aag gac att cga gaa tct gtc act caa atc atg 1536
 Ala Ile Gln Phe Leu Lys Asp Ile Arg Glu Ser Val Thr Gln Ile Met
 500 505 510

aag aat cct aaa gcg aag acc aca gga atg ggt gcc atc tat ggc atg 1584
 Lys Asn Pro Lys Ala Lys Thr Thr Gly Met Gly Ala Ile Tyr Gly Met
 515 520 525

gcc cag aca act gtt gac agg aat atg gtt gca gaa ttg tcc tca gtc 1632
 Ala Gln Thr Thr Val Asp Arg Asn Met Val Ala Glu Leu Ser Ser Val
 530 535 540

ttc ttg gac agc ttg tac agc acc gac act gtc acc cag ggc agc cag 1680
 Phe Leu Asp Ser Leu Tyr Ser Thr Asp Thr Val Thr Gln Gly Ser Gln
 545 550 555 560

atg aat ggt tct cca aaa ccc cac tga 1707
 Met Asn Gly Ser Pro Lys Pro His *
 565

<210> 18
 <211> 568
 <212> PRT
 <213> Homo sapiens

<400> 18
 Met Pro Ser Thr Asp Leu Leu Met Leu Lys Ala Phe Glu Pro Tyr Leu
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 Glu Ile Leu Glu Val Tyr Ser Thr Lys Ala Lys Asn Tyr Val Asn Gly
 20 25 30
 His Cys Thr Lys Tyr Glu Pro Trp Gln Leu Ile Ala Trp Ser Val Val
 35 40 45
 Trp Thr Leu Leu Ile Val Trp Gly Tyr Glu Phe Val Phe Gln Pro Glu
 50 55 60
 Ser Leu Trp Ser Arg Phe Lys Lys Lys Cys Phe Lys Leu Thr Arg Lys
 65 70 75 80
 Met Pro Ile Ile Gly Arg Lys Ile Gln Asp Lys Leu Asn Lys Thr Lys
 85 90 95
 Asp Asp Ile Ser Lys Asn Met Ser Phe Leu Lys Val Asp Lys Glu Tyr
 100 105 110
 Val Lys Ala Leu Pro Ser Gln Gly Leu Ser Ser Ser Ala Val Leu Glu
 115 120 125
 Lys Leu Lys Glu Tyr Ser Ser Met Asp Ala Phe Trp Gln Glu Gly Arg
 130 135 140
 Ala Ser Gly Thr Val Tyr Ser Gly Glu Glu Lys Leu Thr Glu Leu Leu
 145 150 155 160
 Val Lys Ala Tyr Gly Asp Phe Ala Trp Ser Asn Pro Leu His Pro Asp
 165 170 175
 Ile Phe Pro Gly Leu Arg Lys Ile Glu Ala Glu Ile Val Arg Ile Ala
 180 185 190

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Cys Ser Leu Phe Asn Gly Gly Pro Asp Ser Cys Gly Cys Val Thr Ser
 195 200 205
 Gly Gly Thr Glu Ser Ile Leu Met Ala Cys Lys Ala Tyr Arg Asp Leu
 210 215 220
 Ala Phe Glu Lys Gly Ile Lys Thr Pro Glu Ile Val Ala Pro Gln Ser
 225 230 235 240
 Ala His Ala Ala Phe Asn Lys Ala Ala Ser Tyr Phe Gly Met Lys Ile
 245 250 255
 Val Arg Val Pro Leu Thr Lys Met Met Glu Val Asp Val Arg Ala Met
 260 265 270
 Arg Arg Ala Ile Ser Arg Asn Thr Ala Met Leu Val Cys Ser Thr Pro
 275 280 285
 Gln Phe Pro His Gly Val Ile Asp Pro Val Pro Glu Val Ala Lys Leu
 290 295 300
 Ala Val Lys Tyr Lys Ile Pro Leu His Val Asp Ala Cys Leu Gly Gly
 305 310 315 320
 Phe Leu Ile Val Phe Met Glu Lys Ala Gly Tyr Pro Leu Glu His Pro
 325 330 335
 Phe Asp Phe Arg Val Lys Gly Val Thr Ser Ile Ser Ala Asp Thr His
 340 345 350
 Lys Tyr Gly Tyr Ala Pro Lys Gly Ser Ser Leu Val Leu Tyr Ser Asp
 355 360 365
 Lys Lys Tyr Arg Asn Tyr Gln Phe Phe Val Asp Thr Asp Trp Gln Gly
 370 375 380
 Gly Ile Tyr Ala Ser Pro Thr Ile Ala Gly Ser Arg Pro Gly Gly Ile
 385 390 395 400
 Ser Ala Ala Cys Trp Ala Ala Leu Met His Phe Gly Glu Asn Gly Tyr
 405 410 415
 Val Glu Ala Thr Lys Gln Ile Ile Lys Thr Ala Arg Phe Leu Lys Ser
 420 425 430
 Glu Leu Glu Asn Ile Lys Gly Ile Phe Val Phe Gly Asn Pro Gln Leu
 435 440 445
 Ser Val Ile Ala Leu Gly Ser Arg Asp Phe Asp Ile Tyr Arg Leu Ser
 450 455 460
 Asn Leu Met Thr Ala Lys Gly Trp Asn Leu Asn Gln Leu Gln Phe Pro
 465 470 475 480
 Pro Ser Ile His Phe Cys Ile Thr Leu Leu His Ala Arg Lys Arg Val
 485 490 495
 Ala Ile Gln Phe Leu Lys Asp Ile Arg Glu Ser Val Thr Gln Ile Met
 500 505 510
 Lys Asn Pro Lys Ala Lys Thr Thr Gly Met Gly Ala Ile Tyr Gly Met
 515 520 525
 Ala Gln Thr Thr Val Asp Arg Asn Met Val Ala Glu Leu Ser Ser Val
 530 535 540
 Phe Leu Asp Ser Leu Tyr Ser Thr Asp Thr Val Thr Gln Gly Ser Gln
 545 550 555 560
 Met Asn Gly Ser Pro Lys Pro His
 565

<210> 19
 <211> 490
 <212> PRT
 <213> Drosophila melanogaster

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<400> 19
Phe Arg Ser Ser Asn Asp Tyr Gly Val Asn Leu Gln Thr Ala Glu Met
1 5 10 15
Trp His His Thr Ile Arg Lys His Lys Arg Gly Asn Gly Ser Ser Ser
20 25 30
Pro Ala Asp Cys Gly Lys Gln Leu Leu Ile Leu Leu Asn Pro Lys Ser
35 40 45
Gly Ser Gly Lys Gly Arg Glu Leu Phe Gln Lys Gln Val Ala Pro Leu
50 55 60
Leu Thr Glu Ala Glu Val Gln Tyr Asp Leu Gln Ile Thr Thr His Pro
65 70 75 80
Gln Tyr Ala Lys Glu Phe Val Arg Thr Arg Arg Asp Leu Leu Thr Arg
85 90 95
Tyr Ser Gly Ile Val Val Ala Ser Gly Asp Gly Leu Phe Tyr Glu Val
100 105 110
Leu Asn Gly Leu Met Glu Arg Met Asp Trp Arg Arg Ala Cys Arg Glu
115 120 125
Leu Pro Leu Gly Ile Ile Pro Cys Gly Ser Gly Asn Gly Leu Ala Lys
130 135 140
Ser Val Ala His His Cys Asn Glu Pro Tyr Glu Pro Lys Pro Ile Leu
145 150 155 160
His Ala Thr Leu Thr Cys Met Ala Gly Lys Ser Thr Pro Met Asp Val
165 170 175
Val Arg Val Glu Leu Ala Thr Arg Asp Lys His Phe Val Met Tyr Ser
180 185 190
Phe Leu Ser Val Gly Trp Gly Leu Ile Ala Asp Ile Asp Ile Glu Ser
195 200 205
Glu Arg Leu Arg Ser Ile Gly Ala Gln Arg Phe Thr Leu Trp Ala Ile
210 215 220
Lys Arg Leu Ile Gly Leu Arg Ser Tyr Lys Gly Arg Val Ser Tyr Leu
225 230 235 240
Leu Gly Lys Gly Lys Lys Glu Pro Pro Val Glu Ala Ala Arg Glu Leu
245 250 255
Pro Ala Glu Ser Thr Ala Ala Gly Ile Arg Ser Ser Leu Pro Leu Asn
260 265 270
Ala Gly Glu Phe His Asp Leu Pro Glu Glu Glu Glu Gly Glu Ala Val
275 280 285
Leu Asp Gly Glu Gln Phe Ala Asp Ala Ile Ser Leu Asp Arg Ser Val
290 295 300
Tyr Arg Gln His Ala Asp Ser Trp His Ser Ala Met Ser Arg Arg Thr
305 310 315 320
Ala Tyr Tyr Ser Leu Gly Gly Pro Ser Met Arg Ser Asn Arg Ser Arg
325 330 335
Met Ser Ile Ser Gln Arg Ile Glu Ala Ala Asn Ala Glu Phe Ala Glu
340 345 350
Arg Val Pro Thr Gly Thr Ile Pro Pro Leu Gln Met Pro Leu Leu Ser
355 360 365
Ser Asp Gly Trp Ile Cys Glu Asp Gly Asp Phe Val Met Val His Ala
370 375 380
Ala Tyr Thr Thr His Leu Ser Ser Asp Val Phe Phe Ala Pro Glu Ser
385 390 395 400
Arg Leu Asp Asp Gly Leu Ile Tyr Leu Val Ile Ile Arg Arg Gly Val
405 410 415

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Ser Arg His Gln Leu Leu Asn Phe Met Leu Asn Leu Asn Ala Gly Thr
 420 425 430
 His Leu Pro Ile Gly Glu Asp Pro Phe Ile Lys Val Val Pro Cys Arg
 435 440 445
 Ala Phe Arg Ile Glu Pro Ser Ser Ser Asp Gly Ile Leu Val Val Asp
 450 455 460
 Gly Glu Arg Val Glu Tyr Gly Pro Ile Gln Ala Glu Val Met Pro Gly
 465 470 475 480
 Leu Ile Asn Val Met Thr Thr Ser Gly Gln
 485 490

<210> 20
 <211> 524
 <212> PRT
 <213> Drosophila melanogaster

<400> 20
 Phe Arg Ser Phe Asp Thr Phe Glu Asp Asn Met Arg Glu Ala Asp Arg
 1 5 10 15
 Trp Tyr Arg Ser Leu Arg Trp Gln Leu His Arg Thr Leu Glu Glu Ile
 20 25 30
 Phe Val Ala Pro Thr Val Asp Glu Arg Arg Arg Arg Val Leu Val Leu
 35 40 45
 Leu Asn Pro Lys Ser Gly Ser Gly Asp Ala Arg Glu Val Phe Asn Met
 50 55 60
 His Val Thr Pro Val Leu Asn Glu Ala Glu Val Pro Tyr Asp Leu Tyr
 65 70 75 80
 Val Thr Lys His Ser Asn Phe Ala Ile Glu Phe Leu Ser Thr Arg Cys
 85 90 95
 Leu Asp Ala Trp Cys Cys Val Val Ala Val Gly Gly Asp Gly Leu Phe
 100 105 110
 His Glu Ile Val Asn Gly Leu Leu Gln Arg Gln Asp Trp Ala His Val
 115 120 125
 Leu Pro His Leu Ala Leu Gly Ile Ile Pro Cys Gly Ser Gly Asn Gly
 130 135 140
 Leu Ala Arg Ser Ile Ala His Cys Tyr Asn Lys Pro Val Leu Gly Ala
 145 150 155 160
 Ala Leu Thr Val Ile Ser Gly Arg Ser Ser Pro Met Asp Val Val Arg
 165 170 175
 Val Gln Leu Gln Ser Arg Ser Leu Tyr Ser Phe Leu Ser Ile Gly Trp
 180 185 190
 Gly Leu Ile Ser Asp Val Asp Ile Glu Ser Glu Arg Ile Arg Met Leu
 195 200 205
 Gly Tyr Gln Arg Phe Thr Val Trp Thr Leu Tyr Arg Leu Val Asn Leu
 210 215 220
 Arg Thr Tyr Asn Gly Arg Ile Ser Tyr Leu Leu Thr Asp His Glu Val
 225 230 235 240
 Ser Ser Thr His Ser Ala Thr Gly Tyr Ala Ala Gln Arg Arg Met Gln
 245 250 255
 Ser Ser Arg Ser Cys Asn Thr His Ile Asp Met Leu Asn Gly Pro Ala
 260 265 270
 Pro Ile Tyr His Ser Ser Ala Glu Tyr Leu Pro Gln Glu Phe Ala Asp
 275 280 285

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Val Ile Ser Leu Glu Thr Ser Ile Asn Gln Ser Phe Arg Ser Arg Cys
 290 295 300
 Asp Ser Trp Leu Ser Gly Gly Ser Arg Arg Ser Phe Tyr Tyr Ser Ile
 305 310 315 320
 Ser Glu Ser Ile Tyr His Ser Leu Ala Asp Glu Ser Glu Phe Ala Gly
 325 330 335
 Leu Ala Ala Ala Ser Leu Glu Asn Arg Gln Gln Asn Tyr Gly Pro Ala
 340 345 350
 Ser Glu Leu Pro Asp Leu Asn Glu Pro Leu Ser Glu Asp Gln Gly Trp
 355 360 365
 Leu Val Glu Glu Gly Glu Phe Val Met Met His Ala Val Tyr Gln Thr
 370 375 380
 His Leu Gly Ile Asp Cys His Phe Ala Pro Lys Ala Gln Leu Asn Asp
 385 390 395 400
 Gly Thr Ile Tyr Leu Ile Leu Ile Arg Ala Gly Ile Ser Arg Pro His
 405 410 415
 Leu Leu Ser Phe Leu Tyr Asn Met Ser Ser Gly Thr His Leu Pro Glu
 420 425 430
 Ser His Asp Asp His Val Lys Val Leu Pro Val Arg Ala Phe Arg Leu
 435 440 445
 Glu Pro Tyr Asp Asn His Gly Ile Ile Thr Val Asp Gly Glu Arg Val
 450 455 460
 Glu Phe Gly Pro Leu Gln Ala Glu Val Leu Pro Gly Ile Ala Arg Val
 465 470 475 480
 Met Val Pro Asn Val Ser Thr Phe Arg Phe Gln Ser Ala Thr Leu Gln
 485 490 495
 His Gly Ile Pro Val Cys Ile Pro Val Arg Lys Arg Phe Val Leu Tyr
 500 505 510
 Asn Met Ser Ser Glu Glu Leu Ala Pro Ile Asn Glu
 515 520

<210> 21
 <211> 368
 <212> PRT
 <213> Homo sapiens

<400> 21
 Val Leu Val Leu Leu Asn Pro Arg Gly Gly Lys Gly Lys Ala Leu Gln
 1 5 10 15
 Leu Phe Arg Ser His Val Gln Pro Leu Leu Ala Glu Ala Glu Ile Ser
 20 25 30
 Phe Thr Leu Met Leu Thr Glu Arg Arg Asn His Ala Arg Glu Leu Val
 35 40 45
 Arg Ser Glu Glu Leu Gly Arg Trp Asp Ala Leu Val Val Met Ser Gly
 50 55 60
 Asp Gly Leu Met His Glu Val Val Asn Gly Leu Met Glu Arg Pro Asp
 65 70 75 80
 Trp Glu Thr Ala Ile Gln Lys Pro Leu Cys Ser Leu Pro Ala Gly Ser
 85 90 95
 Gly Asn Ala Leu Ala Ala Ser Leu Asn His Tyr Ala Gly Tyr Glu Gln
 100 105 110
 Val Thr Asn Glu Asp Leu Leu Thr Asn Cys Thr Leu Leu Leu Cys Arg
 115 120 125

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Arg	Leu	Leu	Ser	Pro	Met	Asn	Leu	Leu	Ser	Leu	His	Thr	Ala	Ser	Gly
130						135					140				
Leu	Arg	Leu	Phe	Ser	Val	Leu	Ser	Leu	Ala	Trp	Gly	Phe	Ile	Ala	Asp
145					150					155					160
Val	Asp	Leu	Glu	Ser	Glu	Lys	Tyr	Arg	Arg	Leu	Gly	Glu	Met	Arg	Phe
				165					170					175	
Thr	Leu	Gly	Thr	Phe	Leu	Arg	Leu	Ala	Ala	Leu	Arg	Thr	Tyr	Arg	Gly
			180					185					190		
Arg	Leu	Ala	Tyr	Leu	Pro	Val	Gly	Arg	Val	Gly	Ser	Lys	Thr	Pro	Ala
	195						200					205			
Ser	Pro	Val	Val	Val	Gln	Gln	Gly	Pro	Val	Asp	Ala	His	Leu	Val	Pro
	210					215					220				
Leu	Glu	Glu	Pro	Val	Pro	Ser	His	Trp	Thr	Val	Val	Pro	Asp	Glu	Asp
225					230					235					240
Phe	Val	Leu	Val	Leu	Ala	Leu	Leu	His	Ser	His	Leu	Gly	Ser	Glu	Met
				245					250					255	
Phe	Ala	Ala	Pro	Met	Gly	Arg	Cys	Ala	Ala	Gly	Val	Met	His	Leu	Phe
			260					265					270		
Tyr	Val	Arg	Ala	Gly	Val	Ser	Arg	Ala	Met	Leu	Leu	Arg	Leu	Phe	Leu
	275						280					285			
Ala	Met	Glu	Lys	Gly	Arg	His	Met	Glu	Tyr	Glu	Cys	Pro	Tyr	Leu	Val
	290					295				300					
Tyr	Val	Pro	Val	Val	Ala	Phe	Arg	Leu	Glu	Pro	Lys	Asp	Gly	Lys	Gly
305					310					315					320
Val	Phe	Ala	Val	Asp	Gly	Glu	Leu	Met	Val	Ser	Glu	Ala	Val	Gln	Gly
				325					330					335	
Gln	Val	His	Pro	Asn	Tyr	Phe	Trp	Met	Val	Ser	Gly	Cys	Val	Glu	Pro
			340					345					350		
Pro	Pro	Ser	Trp	Lys	Pro	Gln	Gln	Met	Pro	Pro	Pro	Glu	Glu	Pro	Leu
		355					360					365			

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